www.fact-index.com/p/pr/protein_folding.html

Protein folding

Protein folding is the process by which a protein assumes its functional shape or conformation. All protein molecules are simple unbranched chains of amino acids, but it is by coiling into a specific three-dimensional shape that they are able to perform their biological function. In fact, disruption of the functional or "native" shapes of proteins is the primary cause of several neurodegenerative diseases, including those caused by prions and amyloid.

The particular amino-acid sequence of a protein predisposes it to fold into its native conformation, and many proteins do so spontaneously during or after their synthesis inside cells. While these macromolecules may be seen as "folding themselves," in fact their folding depends a great deal on the characteristics of their surrounding solution, including the identity of the primary solvent (either water or lipid inside cells), the concentration of salts, and temperature.

For the most part, scientists have been able to study only many identical molecules folding together *en masse*. It appears that in transitioning to the native state, a given amino acid sequence always takes roughly the same route and proceeds through roughly the same number of fundamental intermediates. At the coarsest level, folding involves first the establishment of secondary structure, particularly alpha helices, and only afterwards tertiary structure (formation of quaternary structure appears to involve the "assembly" or "coassembly" of subunits that have already folded). Shortly before settling into their more stable native conformation, molecules appear to pass additionally through a "molten globule" state. The entire process from fully denatured to fully folded lasts a few tens of milliseconds.

In certain solutions and under some conditions proteins will not fold at all. Temperatures above or below the range that cells tend to live in will cause proteins to unfold or "denature" (this is why boiling makes the white of an egg opaque). High concentrations of solutes and extremes of pH can do the same. A fully denatured protein lacks both tertiary and secondary structure, and exists as a so-called random coil. Cells sometimes protect their proteins against the denaturing influence of heat with enzymes known as chaperones or heat shock proteins, which assist other proteins both in folding and in

remaining folded. Some proteins never fold in cells at all except with the assistance of chaperones. Generally, however, folding is a spontaneous, reversible, equilibrium process.

The determination of the folded structure of a protein is a lengthy and complicated process, involving methods like X-ray crystallography and NMR. In bioinformatics, one of the major areas of interest is the prediction of native structure from amino-acid sequences alone.

Recently a distributed computing application, "folding@home," has been used to simulate protein folding.

See also: Denatured protein

Native conformation
The conformation in which a molecule is biologically active.

www.cartage.org.lb/en/themes/Reference/dictionary/Biologie/N/21.htm

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